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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/843,221A

DATE: 03/13/2002 P.9
TIME: 11:48:58

Input Set : A:\EP.txt
Output Set: N:\CRF3\03132002\I843221A.raw

3 <110> APPLICANT: KOSTENUIK, PAUL
4 LIU, CHUAN-FA
5 LACEY, DAVID LEE
7 <120> TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-

8 RELATED PROTEIN

10 <130> FILE REFERENCE: A-665B
12 <140> CURRENT APPLICATION NUMBER: 09/843,221A
13 <141> CURRENT FILING DATE: 2001-04-26
15 <150> PRIOR APPLICATION NUMBER: 60/266,673
16 <151> PRIOR FILING DATE: 2001-02-06
18 <150> PRIOR APPLICATION NUMBER: 60/214,860
19 <151> PRIOR FILING DATE: 2000-06-28
21 <150> PRIOR APPLICATION NUMBER: 60/200,053
22 <151> PRIOR FILING DATE: 2000-04-27
24 <160> NUMBER OF SEQ ID NOS: 170
26 <170> SOFTWARE: PatentIn version 3.1

28 <210> SEQ ID NO: 1

29 <211> LENGTH: 684

30 <212> TYPE: DNA

31 <213> ORGANISM: Homo sapiens

33 <220> FEATURE:

34 <221> NAME/KEY: CDS

35 <222> LOCATION: (1)..(684)

36 <223> OTHER INFORMATION:

39 <400> SEQUENCE: 1

| | |
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| 40 atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg | 48 |
| 41 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu | |
| 42 1 5 10 15 | |
| 44 ggg-gga-ccg-tca-gtc-ttc-ctc-ttc-ccc-cca-aaa-ccc-aag-gac-acc-ctc | 96 |
| 45 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu | |
| 46 20 25 30 | |
| 48 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc | 144 |
| 49 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser | |
| 50 35 40 45 | |
| 52 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag | 192 |
| 53 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu | |
| 54 50 55 60 | |
| 56 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg | 240 |
| 57 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr | |
| 58 65 70 75 80 | |
| 60 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat | 288 |
| 61 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn | |
| 62 85 90 95 | |

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| | |
|---|-----|
| 64 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc | 336 |
| 65 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro | |
| 66 100 105 110 | |
| 68 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag | 384 |
| 69 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln | |
| 70 115 120 125 | |
| 72 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc | 432 |
| 73 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val | |
| 74 130 135 140 | |
| 76 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg | 480 |
| 77 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val | |
| 78 145 150 155 160 | |
| 80 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct | 528 |
| 81 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Thr Thr Pro | |
| 82 165 170 175 | |
| 84 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc | 576 |
| 85 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr | |
| 86 180 185 190 | |
| 88 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg | 624 |
| 89 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val | |
| 90 195 200 205 | |
| 92 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg | 672 |
| 93 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu | |
| 94 210 215 220 | |
| 96 tct ccg ggt aaa | 684 |
| 97 Ser Pro Gly Lys | |
| 98 225 | |
| 101 <210> SEQ ID NO: 2 | |
| 102 <211> LENGTH: 228 | |
| 103 <212> TYPE: PRT | |
| 104 <213> ORGANISM: Homo sapiens | |
| 106 <400> SEQUENCE: 2 | |
| 108 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu | |
| 109 1 5 10 15 | |
| 112 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu | |
| 113 20 25 30 | |
| 116 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser | |
| 117 35 40 45 | |
| 120 His-Glu-Asp-Pro-Glu-Val-Lys-Phe-Asn-Trp-Tyr-Val-Asp-Gly-Val-Glu | |
| 121 50 55 60 | |
| 124 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr | |
| 125 65 70 75 80 | |
| 128 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn | |
| 129 85 90 95 | |
| 132 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro | |
| 133 100 105 110 | |
| 136 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln | |
| 137 115 120 125 | |
| 140 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val | |

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141      130          135          140
144 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145      145          150          155          160
148 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
149          165          170          175
152 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
153          180          185          190
156 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
157          195          200          205
160 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
161          210          215          220
164 Ser Pro Gly Lys
165 225
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 21
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: PTH/PTHrP
176 <220> FEATURE:
177 <221> NAME/KEY: misc_feature
178 <222> LOCATION: (1)..(1)
179 <223> OTHER INFORMATION: Optional attachment to X3X4X5X6X7, X2X3X4X5X6X7,
X1X2X3X4X5X6X7
180      , or YX1X2X3X4X5X6X7
183 <220> FEATURE:
184 <221> NAME/KEY: misc_feature
185 <222> LOCATION: (1)..(1)
186 <223> OTHER INFORMATION: X8 is an amino acid residue (nonfunctional residue
preferred, M o
187      r Nle most preferred)
190 <220> FEATURE:
191 <221> NAME/KEY: misc_feature
192 <222> LOCATION: (3)..(3)
193 <223> OTHER INFORMATION: X10 is an amino acid residue (an acidic or hydrophilic
residue pr
194      eferred, N or D most preferred)
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (4)..(4)
200 <223> OTHER INFORMATION: X11 is an amino acid residue (nonfunctional or basic residue
pref
201      erred, L, R, or K most preferred)
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (5)..(5)
207 <223> OTHER INFORMATION: X12 is an amino acid residue (nonfunctional or aromatic
residue p
208      referred, G, F, or W most preferred)
211 <220> FEATURE:
212 <221> NAME/KEY: misc_feature
213 <222> LOCATION: (7)..(7)
214 <223> OTHER INFORMATION: X14 is an amino acid residue (basic or hydrophilic residue

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prefer
215 red, H or S most preferred)

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218 <220> FEATURE:
219 <221> NAME/KEY: misc_feature
220 <222> LOCATION: (8)..(8)
221 <223> OTHER INFORMATION: X15 is an amino acid residue (nonfunctional residue preferred, wi
222 th L or I most preferred)
225 <220> FEATURE:
226 <221> NAME/KEY: misc_feature
227 <222> LOCATION: (9)..(9)
228 <223> OTHER INFORMATION: X16 is an amino acid residue (nonfunctional or hydrophilic residu
229 e preferred, Q, N, S, or A most preferred)
232 <220> FEATURE:
233 <221> NAME/KEY: misc_feature
234 <222> LOCATION: (10)..(10)
235 <223> OTHER INFORMATION: X17 is an amino acid residue (acidic, hydrophilic, or nonfunction
236 al residue preferred, S, D, or L most preferred)
239 <220> FEATURE:
240 <221> NAME/KEY: misc_feature
241 <222> LOCATION: (11)..(11)
242 <223> OTHER INFORMATION: X18 is an amino acid residue (nonfunctional residue preferred, M,
243 L, V or Nle most preferred)
246 <220> FEATURE:
247 <221> NAME/KEY: misc_feature
248 <222> LOCATION: (12)..(12)
249 <223> OTHER INFORMATION: X19 is an amino acid residue (acidic or basic residue preferred,
res
250 E or R most preferred)
253 <220> FEATURE:
254 <221> NAME/KEY: misc_feature
255 <222> LOCATION: (14)..(14)
256 <223> OTHER INFORMATION: X21 is an amino acid residue (nonfunctional residue or basic
res
257 idue preferred; V, M, R, or Nle most preferred)
260 <220> FEATURE:
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: (15)..(15)
263 <223> OTHER INFORMATION: X22 is an amino acid residue (hydrophilic, acidic, or aromatic r
264 esidue preferred, E or F most preferred)
267 <220> FEATURE:
268 <221> NAME/KEY: misc_feature
269 <222> LOCATION: (16)..(16)
270 <223> OTHER INFORMATION: X23 is an aromatic or lipophilic residue (W or F preferred)
273 <220> FEATURE:
274 <221> NAME/KEY: misc_feature
275 <222> LOCATION: (17)..(17)
276 <223> OTHER INFORMATION: X24 is a lipophilic residue (L preferred)
279 <220> FEATURE:
280 <221> NAME/KEY: misc_feature
281 <222> LOCATION: (18)..(18)

282 <223> OTHER INFORMATION: X25 is an amino acid residue (hydrophilic or basic residue
prefe
283 rred, R or H most preferred)
286 <220> FEATURE:

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287 <221> NAME/KEY: misc_feature
 288 <222> LOCATION: (19)..(19)
 289 <223> OTHER INFORMATION: X26 is an amino acid residue (hydrophilic or basic residue
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 290 rred, K or H most preferred)
 293 <220> FEATURE:
 294 <221> NAME/KEY: misc_feature
 295 <222> LOCATION: (20)..(20)
 296 <223> OTHER INFORMATION: X27 is an amino acid residue (lipophilic, basic, or
 nonfunctiona
 297 l residue preferred, K or L most preferred)
 300 <220> FEATURE:
 301 <221> NAME/KEY: misc_feature
 302 <222> LOCATION: (21)..(21)
 303 <223> OTHER INFORMATION: X28 is an amino acid residue (lipophilic or nonfunctional
 residu
 304 e preferred, L or I most preferred)
 307 <220> FEATURE:
 308 <221> NAME/KEY: misc_feature
 309 <222> LOCATION: (21)..(21)
 310 <223> OTHER INFORMATION: Optional attachment to X29, X29X30, X29X30X31, X29X30
 X31X32, X29
 311 X30X31X32X33, X29X30X31X32X33X34, X29X30X31X32X33X34X35, or X29X
 312 30X31X32X33X34X35X36
 315 <400> SEQUENCE: 3
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 318 1 5 10 15
 W--> 321 Xaa Xaa Xaa Xaa Xaa
 322 20
 325 <210> SEQ ID NO: 4
 326 <211> LENGTH: 22
 327 <212> TYPE: PRT
 328 <213> ORGANISM: Artificial Sequence
 330 <220> FEATURE:
 331 <223> OTHER INFORMATION: PTH/PTHrP
 333 <220> FEATURE:
 334 <221> NAME/KEY: misc_feature
 335 <222> LOCATION: (1)..(1)
 336 <223> OTHER INFORMATION: Optional attachment to J1J2J3J4J5J6, J2J3J4J5J6, J3J4J5J6
 339 <220> FEATURE:
 340 <221> NAME/KEY: misc_feature
 341 <222> LOCATION: (1)..(1)
 342 <223> OTHER INFORMATION: J7 is an amino acid residue (nonfunctional or aromatic
 residue pr
 343 eferred, L or F most preferred)
 346 <220> FEATURE:
 347 <221> NAME/KEY: misc_feature
 348 <222> LOCATION: (2)..(2)
 349 <223> OTHER INFORMATION: J8 is an amino acid residue (nonfunctional residue
 preferred, M o
 350 r Nle most preferred)
 353 <220> FEATURE:
 354 <221> NAME/KEY: misc_feature

355 <222> LOCATION: (6)..(6)

356 <223> OTHER INFORMATION: J12 is an amino acid residue (nonfunctional or aromatic residue p

VERIFICATION SUMMARY
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Input Set : A:\EP.txt
Output Set: N:\CRF3\03132002\I843221A.raw

L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5